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SEQUENCE LISTING

<110> YEH, EDWARD T.H.
<120> COMPOSITIONS AND USES FOR A NOVEL CELL-DEATH-PROTECTING
PROTEIN

<130> UTSH:248
<140> 09/484,964

<150> 08/964,162
<151> 1997-11-04

<150> 60/030,302
<151> 1996-11-05

<160> 16
<170> PatentIn Ver. 2.0

<210> 1
<211> 1465
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (88)..(390)
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Met Ser Asp Gln Glu Ala Lys Pro Ser
1 5
act gag gac ttg ggg gat aag aag caa ggt gaa tat att aaa ctc aaa 162
Thr Glu Asp Leu Gly Asp Lys Lys Gln Gly Glu Tyr Ile Lys Leu Lys 25
10 15 20
gtc att gga cag gat agc agt gag att cac ttc aaa gtg aaa atg aca 210
Val Ile Gly Gln Asp Ser Ser Glu Ile His Phe Lys Val Lys Met Thr 40
30 35 40
aca cat ctc aag aaa ctc aaa gaa tca tac tgt caa aga cag ggt gtt 258
Thr His Leu Lys Lys Leu Lys Glu Ser Tyr Cys Gln Arg Gln Gly Val 55
45 50 55
cca atg aat tca ctc agg ttt ctc ttt gag ggt cag aga att gct gat 306
Pro Met Asn Ser Leu Arg Phe Leu Phe Glu Gly Gln Arg Ile Ala Asp 70
60 65 70
aat cat act cca aaa gaa ctg gga atg gag gaa gaa gat gtg att gaa 354
Asn His Thr Pro Lys Glu Leu Gly Met Glu Glu Glu Asp Val Ile Glu 85
75 80 85
gtt tat cag gaa caa acg ggg ggt cat tca aca gtt tagatattct 400
Val Tyr Gln Glu Gln Thr Gly Gly His Ser Thr Val 100
90 95 100
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gtgggtgttca aaacggaatt gaaaactggc accccatctc ttgaaacat ctggtaattt 520
gaattctagt gctcattatt cattattgtt tggtttcatt gtgctgattt ttggtgatca 580
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<210> 2
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 2
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 1 5 10 15
 Lys Gln Gly Glu Tyr Ile Lys Leu Lys Val Ile Gly Gln Asp Ser Ser
 20 25 30
 Glu Ile His Phe Lys Val Lys Met Thr Thr His Leu Lys Lys Leu Lys
 35 40 45
 Glu Ser Tyr Cys Gln Arg Gln Gly Val Pro Met Asn Ser Leu Arg Phe
 50 55 60
 Leu Phe Glu Gly Gln Arg Ile Ala Asp Asn His Thr Pro Lys Glu Leu
 65 70 75 80
 Gly Met Glu Glu Glu Asp Val Ile Glu Val Tyr Gln Glu Gln Thr Gly
 85 90 95
 Gly His Ser Thr Val
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<210> 3
 <211> 774
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> modified_base
 <222> (53)
 <223> Y = C or T
 <220>
 <221> modified_base
 <222> (689)
 <223> N = A, C, G or T
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 <221> modified_base
 <222> (739)
 <223> N = A, C, G or T
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 <221> modified_base
 <222> (744)
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cagtttaaga ttaagaggca tacaccactt agtaaaactaa tgaaagccta ttgtgaacga 240
cagggattgt caatgaggca gacagattc cgatttgacg ggcaaccaat caatgaaaca 300
gacacacctg cacagttgga aatggaggat gaagatacaa ttgatgtgtt ccaacagcag 360
acggggagggtg tctactgaaa agggaaacctg cttctttact ccagaactct gttcttttaa 420
gaccaagatt acattctcaa ttagaaaact gcaatttggt tccaccacat cctgactact 480
accgtatagt tttctctatt ctttcatttc ccccttcccc attcctttat tgtacataaa 540
gtaactggta tatgtgcaca agcatattgc attttttttt tttttaacta aacagccaat 600
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<210> 4
 <211> 95
 <212> PRT
 <213> Homo sapiens

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<400> 4
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      20          25          30
Lys Ile Lys Arg His Thr Pro Leu Ser Lys Leu Met Lys Ala Tyr Cys
      35          40          45
Glu Arg Gln Gly Leu Ser Met Arg Gln Ile Arg Phe Arg Phe Asp Gly
      50          55          60
Gln Pro Ile Asn Glu Thr Asp Thr Pro Ala Gln Leu Glu Met Glu Asp
      65          70          75          80
Glu Asp Thr Ile Asp Val Phe Gln Gln Gln Thr Gly Gly Val Tyr
      85          90          95

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<210> 5
 <211> 1733
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> modified_base
 <222> (19)
 <223> N = A, C, G or T

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tgtgaagaca gagaatgacc acatcaacct gaaggtggcc gggcaggacg gctccgtggt 180
gcagttcaag atcaagaggc acacgtcgct gagcaagctg atgaaggcct actgcgagag 240
gcagggcttg tcaatgaggc agatcagatt caggttcgac gggcagccaa tcaatgaaac 300
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gcccgggccg tccatcctcg cattgctgtt gaatggtgag cacgtgacca tgccgaccac 480
aaaggtgtct gcggaaaactc gaggacattc accacgatga ttttctctc tttgatgtac 540
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gctcatttgt gttttccccc cctcctacaa cattttttta accccaaaat tatagcctga 720
atgttcgctt ttagtctggc cagggatctg actcctgagt tggttgcctc tcccctgctc 780
actccagtca catagagaat tgggtgttcc cgcagtggg attgcagctg ttggacaggt 840
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 gtgctctctg gccctcaagc atgtaacctc ggggtctgag gccaggacc caccctctg 1080
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 gtctatacat aaaaaagtaa gactaagtat tgctgaattt gcagttatgt tgcgtgtat 1320
 aagagctact tccaagtgtg gttacaaatg aaccatgga atgatgactt catgttcttc 1380
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<210> 6
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 6
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 Ile Asn Leu Lys Val Ala Gly Gln Asp Gly Ser Val Val Gln Phe Lys
 20 25 30
 Ile Lys Arg His Thr Ser Leu Ser Lys Leu Met Lys Ala Tyr Cys Glu
 35 40 45
 Arg Gln Gly Leu Ser Met Arg Gln Ile Arg Phe Arg Phe Asp Gly Gln
 50 55 60
 Pro Ile Asn Glu Thr Asp Thr Pro Ala Gln Leu Arg Met Glu Asp Glu
 65 70 75 80
 Asp Thr Ile Asp Val Phe Gln Gln Gln Thr Gly Gly Val Pro Glu Ser
 85 90 95
 Ser Leu Ala Gly His Ser Phe
 100

<210> 7
 <211> 9
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Synthetic
 Peptide

<400> 7
 Arg Gly Ser His His His His His His
 1 5

<210> 8
 <211> 30
 <212> DNA
 <213> Homo sapiens

<400> 8
 cttaggatcc atggcctcgg aagacattgc

<210> 9

<211> 30
 <212> DNA
 <213> Homo sapiens

<400> 9
 gtgtgaattc tagacctgtg acagcgtctg

30

<210> 10
 <211> 7
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Synthetic
 Peptide

<400> 10
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<210> 11
 <211> 9
 <212> PRT
 <213> Influenza virus

<400> 11
 Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
 1 5

<<210> 12
 <211> 4
 <212> PRT
 <213> Homo sapiens

<400> 12
 His Ser Thr Val
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210> 13
 <211> 101
 <212> PRT
 <213> Saccharomyces cerevisiae

<400> 13
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 1 5 10 15
 Glu Val Lys Pro Glu Thr His Ile Asn Leu Lys Val Ser Asp Gly Ser
 20 25 30
 Ser Glu Ile Phe Phe Lys Ile Lys Lys Thr Thr Pro Leu Arg Arg Leu
 35 40 45
 Met Glu Ala Phe Ala Lys Arg Gln Gly Lys Glu Met Asp Ser Leu Arg
 50 55 60
 Phe Leu Tyr Asp Gly Ile Arg Ile Gln Ala Asp Gln Thr Pro Glu Asp
 65 70 75 80
 Leu Asp Met Glu Asp Asn Asp Ile Ile Glu Ala His Arg Glu Gln Ile
 85 90 95
 Gly Gly Ala Thr Tyr

[illegible]

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<400> 15
Met Leu Ile Lys Val Lys Thr Leu Thr Gly Lys Glu Ile Glu Ile Asp
  1          5          10
Ile Glu Pro Thr Asp Lys Val Glu Arg Ile Lys Glu Arg Val Glu Glu
      20          25          30
Lys Glu Gly Ile Pro Pro Gln Gln Arg Leu Ile Tyr Ser Gly Lys
      35          40          45
Gln Met Asn Asp Glu Lys Thr Ala Ala Asp Tyr Lys Ile Leu Gly Gly
      50          55          60
Ser Val Leu His Leu Val Leu Ala Leu Arg Gly Gly
      65          70          75

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<400> 16
Val Gln Asp Leu Ala Gln Leu Val Glu Ala Thr Gly Val Pro Leu
      1      5      10      15
Pro Phe Gln Lys Leu Ile Phe Lys Gly Lys Ser Leu Lys Glu
      20      25      30

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